Amendments to the Claims

1. (*Currently amended*) In a network system for biological exploration and analysis, A a method for managing a plurality of databases containing gene expression data and related data corresponding to a plurality of gene fragments of integrating multiple gene databases containing gene expression data, gene annotation data, and sample data, the method comprising:

storing the gene expression data and the related data in separate databases;

defining new classes and associations for the gene expression and related data, gene annotation data, and sample data contained in at least one of the multiple gene databases;

grouping the plurality of gene fragments into at least two groups gene fragment classes according to at least one attribute of a plurality of attributes of the gene expression data and related data, the plurality of attributes selected from the group consisting of known versus unknown standardized identifier, gene fragment identity, gene sequence, experiment data, sample data, gene pathway, chromosome location, and expression results, wherein sample data includes information corresponding to one or more of donor, organ, tissue, disease, pathology, genomics, medications and preparation, and wherein expression results include information corresponding to one or more of call value, expression level, fold change, up-regulated versus down-regulated; and

annotating gene fragments, using a relational format, generating a plurality of links between the separate databases for linking the gene expression data for each gene fragment to the at least one attribute corresponding to the gene fragment class into which the gene fragment is grouped;

so as to permit a database analytical engine to analyze the gene expression data, gene annotation data contained in the multiple gene databases

wherein a user query comprising a selection of one or a combination of attributes produces a result comprising a subset of the gene expression data and the related data corresponding to one or more gene fragment classes having the selected one or a combination of attributes.

Claims 2 - 14. (*Canceled*)

15. (*New*) The method of Claim 1, wherein the related data is divided into two databases comprising a sample database within which the sample data reside and a gene annotation database within which gene annotation data comprising known versus unknown standardized identifier, gene fragment identity, gene sequence, gene pathway and chromosome location reside.

16. (*New*) The method of Claim 15, wherein the selection of one or more of a combination of attributes comprises:

selecting one or a combination of attributes of the gene annotation data to define a gene set; and

selecting one or a combination of attributes of the sample data to define one or more sample sets;

wherein the result comprises a ranking of the expression levels for each gene fragment within the gene set across the one or more sample sets.

17. (*New*) The method of Claim 1, wherein the selection of one or a combination of attributes comprises defining a sample set and specifying a call value threshold, wherein the result comprises a gene signature analysis to identify a pair of gene sets comprising present genes and absent genes within the sample set.

18. (*New*) The method of Claim 17, further comprising storing the result in a workspace manager, wherein the selection of one or more attributes further comprises:

defining a second sample set and the call value threshold to perform a second gene signature analysis; and

comparing the results for the first and second sample sets to produce a gene signature differential analysis.

19. (*New*) The method of Claim 1, wherein the selection of one or a combination of attributes comprises:

defining each of a control sample set and an experimental sample set; and

comparing expression levels for the control sample set and experimental sample set to produce a fold change analysis.

20. (*New*) The method of Claim 19, wherein the selection of one or a combination of attributes further comprises selecting an additional attribute corresponding to a fold change value threshold.

21. (*New*) A network system for biological exploration and analysis of a plurality of databases containing gene expression data and related data corresponding to a plurality of gene fragments, the system comprising:

an analysis engine;

a gene expression database for storing the gene expression data;

at least one separate database for storing the related data;

a common interface for linking the gene expression data and the related data by:

grouping the plurality of gene fragments into at least two gene fragment classes according to at least one attribute of a plurality of attributes of the gene expression data and related data, the plurality of attributes selected from the group consisting of known versus unknown standardized identifier, gene fragment identity, gene sequence, experiment data, sample data, gene pathway, chromosome location, and expression results, wherein sample data includes information corresponding to one or more of donor, organ, tissue, disease, pathology, genomics, medications and preparation, and wherein expression results include information corresponding to one or more of call value, expression level, fold change, up-regulated versus down-regulated; and

using a relational format, generating a plurality of links between the gene expression database and the at least one separate database for associating the gene expression data for each gene fragment to the at least one attribute corresponding to the gene fragment class into which the gene fragment is grouped; and

a user interface for entry of a user query and reporting of a result, wherein the user query comprises a selection of one or a combination of attributes for directing the analysis engine to search the gene expression database and the at least one separate data database for a

subset of the gene expression data and the related data corresponding to one or more gene fragment classes having the selected one or a combination of attributes.

22. (*New*) The system of Claim 21, wherein the at least one separate database comprises a sample database within which the sample data reside and a gene annotation database within which gene annotation data reside.

23. (*New*) The system of Claim 22, wherein the gene annotation data comprises one or more of known versus unknown standardized identifier, gene fragment identity, gene sequence, gene pathway and chromosome location.

24. (*New*) The system of Claim 22, wherein the user query comprises:

selecting one or a combination of attributes of the gene annotation data to define a gene set; and

selecting one or a combination of attributes of the sample data to define one or more sample sets;

wherein the result comprises a ranking of the expression levels for each gene fragment within the gene set across the one or more sample sets.

25. (*New*) The system of Claim 21, wherein the user query comprises selection of a combination of attributes to define a sample set and to specify a call value threshold, wherein the result comprises a gene signature analysis to identify a pair of gene sets comprising present genes and absent genes within the sample set.

26. (*New*) The system of Claim 25, further comprising a workspace manager for storing the result, wherein the user query further comprises:

defining a second sample set and the call value threshold to perform a second gene signature analysis; and

comparing the results for the first and second sample sets to produce a gene signature differential analysis.

27. (*New*) The system of Claim 21, wherein the user query comprises:

selecting one or a combination of attributes defining each of a control sample set and an experimental sample set; and

comparing expression levels for the control sample set and experimental sample set to produce a fold change analysis.

28. (*New*) The system of Claim 27, wherein user query further comprises selection of an additional attribute corresponding to a fold change value threshold.

29. (*New*) A computer program product comprising a computer-usable medium having computer-readable program code embodied thereon relating to a plurality of databases containing gene expression data and related data corresponding to a plurality of gene fragments, the computer program product comprising computer-readable program code for effecting the following steps within a computing system:

dividing the gene expression data and the related data into separate databases;

grouping the plurality of gene fragments into at least two gene fragment classes according to at least one attribute of a plurality of attributes of the gene expression data and related data, the plurality of attributes selected from the group consisting of known versus unknown standardized identifier, gene fragment identity, gene sequence, experiment data, sample data, gene pathway, chromosome location, and expression results, wherein sample data includes information corresponding to one or more of donor, organ, tissue, disease, pathology, genomics, medications and preparation, and wherein expression results include information corresponding to one or more of call value, expression level, fold change, up-regulated versus down-regulated; and

using a relational format, generating a plurality of links between the separate databases for linking the gene expression data for each gene fragment to the at least one attribute corresponding to the gene fragment class into which the gene fragment is grouped;

wherein a user query comprising a selection of one or a combination of attributes produces a result comprising a subset of the gene expression data and the related data corresponding to one or more gene fragment classes having the selected one or a combination of attributes.

30. (*New*) The computer program product of claim 29, wherein the related data is divided among a sample database within which the sample data reside and a gene annotation database within which gene annotation data comprising known versus unknown standardized identifier, gene fragment identity, gene sequence, gene pathway and chromosome location reside.

31. (*New*) The computer program product of Claim 30, wherein the selection of one or more of a combination of attributes comprises:

selecting one or a combination of attributes of the gene annotation data to define a gene set; and

selecting one or a combination of attributes of the sample data to define one or more sample sets;

wherein the result comprises a ranking of the expression levels for each gene fragment within the gene set across the one or more sample sets.

32. (*New*) The computer program product of Claim 29, wherein the selection of one or a combination of attributes comprises defining a sample set and specifying a call value threshold, wherein the result comprises a gene signature analysis to identify a pair of gene sets comprising present genes and absent genes within the sample set.

33. (*New*) The computer program product of Claim 32, further operable for effecting storage of the result in a workspace manager, wherein the selection of one or more attributes further comprises:

defining a second sample set and the call value threshold to perform a second gene signature analysis; and

comparing the results for the first and second sample sets to produce a gene signature differential analysis.

34. (*New*) The method of Claim 29, wherein the selection of one or a combination of attributes comprises:

defining each of a control sample set and an experimental sample set; and

comparing expression levels for the control sample set and experimental sample set to produce a fold change analysis.

35. (*New*) In a network system for biological exploration and analysis, a plurality of databases containing data corresponding to a plurality of gene fragments, the plurality of databases comprising:

a gene expression database for storing the gene expression data corresponding to the plurality of gene fragments;

a sample database for storing sample data corresponding to the gene expression data; and

a gene annotation database for storing gene annotation data corresponding to the gene expression data;

wherein the gene expression database, the sample database and the gene annotation database are linked by grouping the plurality of gene fragments into at least two gene fragment classes according to at least one attribute of a plurality of attributes of the gene expression data, the sample data and the gene annotation data, the plurality of attributes selected from the group consisting of known versus unknown standardized identifier, gene fragment identity, gene sequence, experiment data, sample data, gene pathway, chromosome location, and expression results, wherein sample data includes information corresponding to one or more of donor, organ, tissue, disease, pathology, genomics, medications and preparation, and wherein expression results include information corresponding to one or more of call value, expression level, fold change, up-regulated versus down-regulated, and wherein a user query entered into the network system comprises a selection of one or a combination of attributes for searching the gene expression database, the sample database and the gene annotation database for a subset of the gene expression data and the sample data and the gene annotation data corresponding to one or more gene fragment classes having the selected one or a combination of attributes.

36. (*New*) The system of Claim 35, wherein the gene annotation data comprises one or more of known versus unknown standardized identifier, gene fragment identity, gene sequence, gene pathway and chromosome location.

37. (*New*) The system of Claim 35, wherein the user query comprises:

selecting one or a combination of attributes of the gene annotation data to define a gene set; and

selecting one or a combination of attributes of the sample data to define one or more sample sets;

wherein the result comprises a ranking of the expression levels for each gene fragment within the gene set across the one or more sample sets.

38. (*New*) The system of Claim 35, wherein the user query comprises selection of a combination of attributes to define a sample set and to specify a call value threshold, wherein the result comprises a gene signature analysis to identify a pair of gene sets comprising present genes and absent genes within the sample set.

39. (*New*) The system of Claim 38, further comprising a workspace manager for storing the result, wherein the user query further comprises:

defining a second sample set and the call value threshold to perform a second gene signature analysis; and

comparing the results for the first and second sample sets to produce a gene signature differential analysis.

40. (*New*) The system of Claim 35, wherein the user query comprises:

selecting one or a combination of attributes defining each of a control sample set and an experimental sample set; and

comparing expression levels for the control sample set and experimental sample set to produce a fold change analysis.

41. (*New*) The system of Claim 40, wherein user query further comprises selection of an additional attribute corresponding to a fold change value threshold.